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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=2; day=5; hr=15; min=52; sec=47; ms=712;]

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Reviewer Comments:

<120> COMPRISING OF POLYPEPTIDES SPECIFIC TO PATHOGENIC STRAINS AND
THEIR
USE AS VACCINES AND IN IMMUNOTHERAPY

The first line of the above <120> response exceeds the Sequence Rules' required 72-character limit (this includes white spaces). Please insert a hard return after "PATHOGENIC."

(from Sequence 5)

Ser Lys Thr Val Thr Pro Gly Leu His Tyr Ala Ala Asp Gly Phe Arg

770

775

780

Please remove the blank line between the above amino acids and their respective numbers. This error also appears in Sequences 8, 34, 43, 50, 62, 139, and 159.

(also from Sequence 5)

Ser Gly Lys Gln Phe Ser Trp Lys Asp Gln Gly Met Asn Leu Thr
1175 1180 1185

Met Lys Asp Lys Asp Phe Asn Pro Leu Ile Gly Arg Thr Gly Val

Please remove the series of blank lines above, that appear between the

amino acid numbers and the succeeding amino acid line. Only one line should separate them.

(from Sequence 160)

gatattaata aaaatctgcg tcttaatgtc ggcgtcagta atatcctcaa taaacagatc 2100

ttccgatctt ctgaaggggc gaatacctat aacgagccag gccgggctta ttatgccgga 2160

gttaccgcat cattc 2175

130

Please remove the above series of blank lines between the last two nucleotide lines. Only one line should separate them. Also, please remove the "130" above, which appears at the end of the submitted file.

Application No: 10594461

Version No: 1.0

Input Set:**Output Set:**

Started: 2007-12-09 13:44:02.663
Finished: 2007-12-09 13:44:11.804
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 141 ms
Total Warnings: 0
Total Errors: 19
No. of SeqIDs Defined: 160
Actual SeqID Count: 160

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (34)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (43)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (50)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (62)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (139)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (159)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (160)

SEQUENCE LISTING

<110> MUTABILIS

<120> COMPRISING OF POLYPEPTIDES SPECIFIC TO PATHOGENIC STRAINS AND THEIR
USE AS VACCINES AND IN IMMUNOTHERAPY

<130> 1721-126

<140> 10594461

<141> 2007-12-09

<160> 160

<170> PatentIn version 3.1

<210> 1

<211> 163

<212> PRT

<213> Escherichia coli

<400> 1

Met	Lys	Leu	Lys	Ala	Ile	Ile	Leu	Ala	Thr	Gly	Leu	Ile	Asn	Cys	Ile
1				5					10					15	

Val	Phe	Ser	Ala	Gln	Ala	Val	Asp	Thr	Thr	Ile	Thr	Val	Thr	Gly	Asn
			20					25						30	

Val	Leu	Gln	Arg	Thr	Cys	Asn	Val	Pro	Gly	Asn	Val	Asp	Val	Ser	Leu
		35					40					45			

Gly	Asn	Leu	Tyr	Val	Ser	Asp	Phe	Pro	Asn	Ala	Gly	Ser	Gly	Ser	Pro
	50					55					60				

Trp	Val	Asn	Phe	Asp	Leu	Ser	Leu	Thr	Gly	Cys	Gln	Asn	Met	Asn	Thr
65					70					75				80	

Val	Arg	Ala	Thr	Phe	Ser	Gly	Thr	Ala	Asp	Gly	Gln	Thr	Tyr	Tyr	Ala
			85						90					95	

Asn	Thr	Gly	Asn	Ala	Gly	Gly	Ile	Lys	Ile	Glu	Ile	Gln	Asp	Arg	Asp
		100						105					110		

Gly	Ser	Asn	Ala	Ser	Tyr	His	Asn	Gly	Met	Phe	Lys	Thr	Leu	Asn	Val
		115					120					125			

Gln	Asn	Asn	Asn	Ala	Thr	Phe	Asn	Leu	Lys	Ala	Arg	Ala	Val	Ser	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130

135

140

Gly Gln Val Thr Pro Gly Asn Ile Ser Ser Val Ile Thr Val Thr Tyr
 145 150 155 160

Thr Tyr Ala

<210> 2

<211> 673

<212> PRT

<213> Escherichia coli

<400> 2

Met Lys Met Thr Arg Leu Tyr Pro Leu Ala Leu Gly Gly Leu Leu Leu
 1 5 10 15

Pro Ala Ile Ala Asn Ala Gln Thr Ser Gln Gln Asp Glu Ser Thr Leu
 20 25 30

Val Val Thr Ala Ser Lys Gln Ser Ser Arg Ser Ala Ser Ala Asn Asn
 35 40 45

Val Ser Ser Thr Val Val Ser Ala Pro Glu Leu Ser Asp Ala Gly Val
 50 55 60

Thr Ala Ser Asp Lys Leu Pro Arg Val Leu Pro Gly Leu Asn Ile Glu
 65 70 75 80

Asn Ser Gly Asn Met Leu Phe Ser Thr Ile Ser Leu Arg Gly Val Ser
 85 90 95

Ser Ala Gln Asp Phe Tyr Asn Pro Ala Val Thr Leu Tyr Val Asp Gly
 100 105 110

Val Pro Gln Leu Ser Thr Asn Thr Ile Gln Ala Leu Thr Asp Val Gln
 115 120 125

Ser Val Glu Leu Leu Arg Gly Pro Gln Gly Thr Leu Tyr Gly Lys Ser
 130 135 140

Ala Gln Gly Gly Ile Ile Asn Ile Val Thr Gln Gln Pro Asp Ser Thr
 145 150 155 160

Pro Arg Gly Tyr Ile Glu Gly Gly Val Ser Ser Arg Asp Ser Tyr Arg		
165	170	175
Ser Lys Phe Asn Leu Ser Gly Pro Ile Gln Asp Gly Leu Leu Tyr Gly		
180	185	190
Ser Val Thr Leu Leu Arg Gln Val Asp Asp Gly Asp Met Ile Asn Pro		
195	200	205
Ala Thr Gly Ser Asp Asp Leu Gly Gly Thr Arg Ala Ser Ile Gly Asn		
210	215	220
Val Lys Leu Arg Leu Ala Pro Asp Asp Gln Pro Trp Glu Met Gly Phe		
225	230	235 240
Ala Ala Ser Arg Glu Cys Thr Arg Ala Thr Gln Asp Ala Tyr Val Gly		
245	250	255
Trp Asn Asp Ile Lys Gly Arg Lys Leu Ser Ile Ser Asp Gly Ser Pro		
260	265	270
Asp Pro Tyr Met Arg Arg Cys Thr Asp Ser Gln Thr Leu Ser Gly Lys		
275	280	285
Tyr Thr Thr Asp Asp Trp Val Phe Asn Leu Ile Ser Ala Trp Gln Gln		
290	295	300
Gln His Tyr Ser Arg Thr Phe Pro Ser Gly Ser Leu Ile Val Asn Met		
305	310	315 320
Ser Gln Arg Trp Asn Gln Asp Val Gln Glu Leu Arg Ala Ala Thr Leu		
325	330	335
Gly Asp Ala Arg Thr Val Asp Met Val Phe Gly Leu Tyr Arg Gln Asn		
340	345	350
Thr Arg Glu Lys Leu Asn Ser Ala Tyr Asp Met Pro Thr Met Pro Tyr		
355	360	365
Leu Ser Ser Thr Gly Tyr Thr Thr Ala Glu Thr Leu Ala Ala Tyr Ser		
370	375	380

Asp Leu Thr Trp His Leu Thr Asp Arg Phe Asp Ile Gly Gly Gly Val
385 390 395 400

Arg Phe Ser His Asp Lys Ser Ser Thr Gln Tyr His Gly Ser Met Leu
405 410 415

Gly Asn Pro Phe Gly Asp Gln Gly Lys Ser Asn Asp Asp Gln Val Leu
420 425 430

Gly Gln Leu Ser Ala Gly Tyr Met Leu Thr Asp Asp Trp Arg Val Tyr
435 440 445

Thr Arg Val Ala Gln Gly Tyr Lys Pro Ser Gly Tyr Asn Ile Val Pro
450 455 460

Thr Ala Gly Leu Asp Ala Lys Pro Phe Val Ala Glu Lys Ser Ile Asn
465 470 475 480

Tyr Glu Leu Gly Thr Arg Tyr Glu Thr Ala Asp Val Thr Leu Gln Ala
485 490 495

Ala Thr Phe Tyr Thr His Thr Lys Asp Met Gln Leu Tyr Ser Gly Pro
500 505 510

Val Gly Met Gln Thr Leu Ser Asn Ala Gly Lys Ala Asp Ala Thr Gly
515 520 525

Val Glu Leu Glu Ala Lys Trp Arg Phe Ala Pro Gly Trp Ser Trp Asp
530 535 540

Ile Asn Gly Asn Val Ile Arg Ser Glu Phe Thr Asn Asp Ser Glu Leu
545 550 555 560

Tyr His Gly Asn Arg Val Pro Phe Val Pro Arg Tyr Gly Ala Gly Ser
565 570 575

Ser Val Asn Gly Val Ile Asp Thr Arg Tyr Gly Ala Leu Met Pro Arg
580 585 590

Leu Ala Val Asn Leu Val Gly Pro His Tyr Phe Asp Gly Asp Asn Gln
595 600 605

Leu Arg Gln Gly Thr Tyr Ala Thr Leu Asp Ser Ser Leu Gly Trp Gln

610

615

620

Ala Thr Glu Arg Met Asn Ile Ser Val Tyr Val Asp Asn Leu Phe Asp
625 630 635 640

Arg Arg Tyr Arg Thr Tyr Gly Tyr Met Asn Gly Ser Ser Ala Val Ala
645 650 655

Gln Val Asn Met Gly Arg Thr Val Gly Ile Asn Thr Arg Ile Asp Phe
660 665 670

Phe

<210> 3

<211> 246

<212> PRT

<213> Escherichia coli

<400> 3

Met Asn Lys Val Phe Val Val Ser Val Val Ala Ala Ala Cys Val Phe
1 5 10 15

Ala Val Asn Ala Gly Ala Lys Glu Gly Lys Ser Gly Phe Tyr Leu Thr
20 25 30

Gly Lys Ala Gly Ala Ser Val Met Ser Leu Ser Asp Gln Arg Phe Leu
35 40 45

Ser Gly Asp Glu Glu Glu Thr Ser Lys Tyr Lys Gly Gly Asp Asp His
50 55 60

Asp Thr Val Phe Ser Gly Gly Ile Ala Val Gly Tyr Asp Phe Tyr Pro
65 70 75 80

Gln Phe Ser Ile Pro Val Arg Thr Glu Leu Glu Phe Tyr Ala Arg Gly
85 90 95

Lys Ala Asp Ser Lys Tyr Asn Val Asp Lys Asp Ser Trp Ser Gly Gly
100 105 110

Tyr Trp Arg Asp Asp Leu Lys Asn Glu Val Ser Val Asn Thr Leu Met
115 120 125

Leu Asn Ala Tyr Tyr Asp Phe Arg Asn Asp Ser Ala Phe Thr Pro Trp
130 135 140

Val Ser Ala Gly Ile Gly Tyr Ala Arg Ile His Gln Lys Thr Thr Gly
145 150 155 160

Ile Ser Thr Trp Asp Tyr Glu Tyr Gly Ser Ser Gly Arg Glu Ser Leu
165 170 175

Ser Arg Ser Gly Ser Ala Asp Asn Phe Ala Trp Ser Leu Gly Ala Gly
180 185 190

Val Arg Tyr Asp Val Thr Pro Asp Ile Ala Leu Asp Leu Ser Tyr Arg
195 200 205

Tyr Leu Asp Ala Gly Asp Ser Ser Val Ser Tyr Lys Asp Glu Trp Gly
210 215 220

Asp Lys Tyr Lys Ser Glu Val Asp Val Lys Ser His Asp Ile Met Leu
225 230 235 240

Gly Met Thr Tyr Asn Phe
245

<210> 4
<211> 166
<212> PRT
<213> Escherichia coli

<400> 4

Met Lys Leu Lys Ala Ile Ile Leu Ala Thr Gly Leu Ile Asn Cys Ile
1 5 10 15

Ala Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Arg
20 25 30

Val Leu Pro Arg Thr Cys Thr Ile Gly Asn Gly Gly Asn Pro Asn Ala
35 40 45

Thr Val Val Leu Asp Asn Ala Tyr Thr Ser Asp Leu Ile Ala Ala Asn
50 55 60

Ser Thr Ser Gln Trp Lys Asn Phe Ser Leu Thr Leu Thr Asn Cys Gln
65 70 75 80

Asn Val Asn Asn Val Thr Ser Phe Gly Gly Thr Ala Glu Asn Thr Asn
85 90 95

Tyr Tyr Arg Asn Thr Gly Asp Ala Thr Asn Ile Met Val Glu Leu Gln
100 105 110

Glu Gln Gly Asn Gly Asn Thr Pro Leu Lys Val Gly Ser Thr Lys Val
115 120 125

Val Thr Val Ser Asn Gly Gln Ala Thr Phe Asn Leu Lys Val Arg Ala
130 135 140

Val Ser Lys Gly Asn Ala Gly Ala Gly Ser Ile Asn Ser Gln Ile Thr
145 150 155 160

Val Thr Tyr Thr Tyr Ala
165

<210> 5
<211> 1295
<212> PRT
<213> Escherichia coli

<400> 5

Met Asn Lys Ile Tyr Ser Leu Lys Tyr Ser Ala Ala Thr Gly Gly Leu
1 5 10 15

Ile Ala Val Ser Glu Leu Ala Lys Arg Val Ser Gly Lys Thr Asn Arg
20 25 30

Lys Leu Val Ala Thr Met Leu Ser Leu Ala Val Ala Gly Thr Val Asn
35 40 45

Ala Ala Asn Ile Asp Ile Ser Asn Val Trp Ala Arg Asp Tyr Leu Asp
50 55 60

Leu Ala Gln Asn Lys Gly Ile Phe Gln Pro Gly Ala Thr Asp Val Thr
65 70 75 80

Ile Thr Leu Lys Asn Gly Asp Lys Phe Ser Phe His Asn Leu Ser Ile
85 90 95

Pro Asp Phe Ser Gly Ala Ala Ala Ser Gly Ala Ala Thr Ala Ile Gly
100 105 110

Gly Ser Tyr Ser Val Thr Val Ala His Asn Lys Lys Asn Pro Gln Ala
115 120 125

Ala Glu Thr Gln Val Tyr Ala Gln Ser Ser Tyr Arg Val Val Asp Arg
130 135 140

Arg Asn Ser Asn Asp Phe Glu Ile Gln Arg Leu Asn Lys Phe Val Val
145 150 155 160

Glu Thr Val Gly Ala Thr Pro Ala Glu Thr Asn Pro Thr Thr Tyr Ser
165 170 175

Asp Ala Leu Glu Arg Tyr Gly Ile Val Thr Ser Asp Gly Ser Lys Lys
180 185 190

Ile Ile Gly Phe Arg Ala Gly Ser Gly Gly Thr Ser Phe Ile Asn Gly
195 200 205

Glu Ser Lys Ile Ser Thr Asn Ser Ala Tyr Ser His Asp Leu Leu Ser
210 215 220

Ala Ser Leu Phe Glu Val Thr Gln Trp Asp Ser Tyr Gly Met Met Ile
225 230 235 240

Tyr Lys Asn Asp Lys Thr Phe Arg Asn Leu Glu Ile Phe Gly Asp Ser
245 250 255

Gly Ser Gly Ala Tyr Leu Tyr Asp Asn Lys Leu Glu Lys Trp Val Leu
260 265 270

Val Gly Thr Thr His Gly Ile Ala Ser Val Asn Gly Asp Gln Leu Thr
275 280 285

Trp Ile Thr Lys Tyr Asn Asp Lys Leu Val Ser Glu Leu Lys Asp Thr
290 295 300

Tyr Ser His Lys Ile Asn Leu Asn Gly Asn Asn Val Thr Ile Lys Asn
305 310 315 320

Thr Asp Ile Thr Leu His Gln Asn Asn Ala Asp Thr Thr Gly Thr Gln
325 330 335

Glu Lys Ile Thr Lys Asp Lys Asp Ile Val Phe Thr Asn Gly Gly Asp
340 345 350

Val Leu Phe Lys Asp Asn Leu Asp Phe Gly Ser Gly Gly Ile Ile Phe
355 360 365

Asp Glu Gly His Glu Tyr Asn Ile Asn Gly Gln Gly Phe Thr Phe Lys
370 375 380

Gly Ala Gly Ile Asp Ile Gly Lys Glu Ser Ile Val Asn Trp Asn Ala
385 390 395 400

Leu Tyr Ser Ser Asp Asp Val Leu His Lys Ile Gly Pro Gly Thr Leu
405 410 415

Asn Val Gln Lys Lys Gln Gly Ala Asn Ile Lys Ile Gly Glu Gly Asn
420 425 430

Val Ile Leu Asn Glu Glu Gly Thr Phe Asn Asn Ile Tyr Leu Ala Ser
435 440 445

Gly Asn Gly Lys Val Ile Leu Asn Lys Asp Asn Ser Leu Gly Asn Asp
450 455 460

Gln Tyr Ala Gly Ile Phe Phe Thr Lys Arg Gly Gly Thr Leu Asp Leu
465 470 475 480

Asn Gly His Asn Gln Thr Phe Thr Arg Ile Ala Ala Thr Asp Asp Gly
485 490 495

Thr Thr Ile Thr Asn Ser Asp Thr Thr Lys Glu Ala Val Leu Ala Ile
500 505 510

Asn Asn Glu Asp Ser Tyr Ile Tyr His Gly Asn Ile Asn Gly Asn Ile
515 520 525

Lys Leu Thr His Asn Ile Asn Ser Gln Asp Lys Lys Thr Asn Ala Lys
530 535 540

Leu Ile Leu Asp Gly Ser Val Asn Thr Lys Asn Asp Val Glu Val Ser
545 550 555 560

Asn Ala Ser Leu Thr Met Gln Gly His Ala Thr Glu His Ala Ile Phe
565 570 575

Arg Ser Ser Ala Asn His Cys Ser Leu Val Phe Leu Cys Gly Thr Asp
580 585 590

Trp Val Thr Val Leu Lys Glu Thr Glu Ser Ser Tyr Asn Lys Lys Phe
595 600 605

Asn Ser Asp Tyr Lys Ser Asn Asn Gln Gln Thr Ser Phe Asp Gln Pro
610 615 620

Asp Trp Lys Thr Gly Val Phe Lys Phe Asp Thr Leu His Leu Asn Asn
625 630 635 640

Ala Asp Phe Ser Ile Ser Arg Asn Ala Asn Val Glu Gly Asn Ile Ser
645 650 655

Ala Asn Lys Ser Ala Ile Thr Ile Gly Asp Lys Asn Val Tyr Ile Asp
660 665 670

Asn Leu Ala Gly Lys Asn Ile Thr Asn Asn Gly Phe Asp Phe Lys Gln
675 680 685

Thr Ile Ser Thr Asn Leu Ser Ile Gly Glu Thr Lys Phe Thr Gly Gly
690 695 700

Ile Thr Ala His Asn Ser Gln Ile Ala Ile Gly Asp Gln Ala Val Val
705 710 715 720

Thr Leu Asn Gly Ala Thr Phe Leu Asp Asn Thr Pro Ile Ser Ile Asp
725 730 735

Lys Gly Ala Lys Val Ile Ala Gln Asn Ser Met Phe Thr Thr Lys Gly
740 745